

1/88

SEQUENCE LISTING

<110> Lovejoy, David

Chewpoy, R.B.

Barsyte, Dalia

Rotzinger, Susan

<120> Tereuin C-Terminal Associated Peptides (TCAP)

<130> 2223-159

<150> US 60/376,879

<151> 2002-05-02

<150> US 60/377,231

<151> 2002-05-03

<150> US 60/424,016

<151> 2002-11-06

<160> 136

<170> PatentIn version 3.1

<210> 1

<211> 1490

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout Ten M3 carboxy termini'

2/88

<400> 1  
tccatctcgg ggggtgcaaca ggaagtgacc cggcaagcca aggctttcct gtccttcgag 60  
aggatgccgg agatccagct gagccgccgg cgctccaacc gggagaaaacc ctggctgtgg 120  
ttcgccaccg ccaagtctct gatcggttaag ggtgtcatgt tggcggtgac gcagggccgt 180  
gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggtegc cgccttcctc 240  
aacaatgcgt tctacctgga ggacctgcac ttcacggtgg agggacgcga cacgcactac 300  
ttcatcaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg 360  
aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tggatgaacgg 420  
cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgct ccacgtgcgc 480  
tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg 540  
ttgtcgagtg cctggtccag ggagcaacaa cgggtgaggg agggggagga gggggtgagg 600  
ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac 660  
gggtactacg tcctctccat agagcagtac cccgagctag cagactccgc taacaacatc 720  
cagttcctca ggcagagcga aataggggaag aggtaacaga cagaatcctc ggcactggcc 780  
gccaaagaga ctacccccctc caaatcctgc cccccaacct ccctcgctc ccccttttc 840  
tctaaaaagg gggagggtcc aggctagtgc tgtgttttagc gccgactagc tgaaacaaac 900  
agtaaaatgt agaatatctt aaactgaact atacctaata ctaccactgt ggggcctgaa 960  
aatcaaacaa aacggctcca actgacgcaa atgtttgtcc catgtgctat acagcggtga 1020  
atggactgtg gactctcttg aaaagagaga aaaaaagtc aaaactctcg gtttgtgaaa 1080  
ggagaaaaaa acgttttttt tttttttaa tagacttcct gaatttgctt tcggaaaaaa 1140  
tattttaaaa agaaagaaga aatgtgttta catacgcata aactacaac acgtctggac 1200  
taatagaaga aaagccttct ggtttcttac acaggacaac gtctataatc tgattctaca 1260  
tcctgacgac tgacctttga ttgacctttg cgtactgaaa aaggtagtgt tgttgttcgc 1320  
agtaggacca tgggtctcca atggtggtaa ctagacagtt aaaaccactt gttgaaacca 1380  
cttgcttggt cttctgcttt tctttccaaa agggacaaaa cagctcccac caagtgactt 1440  
ctttaccaat actagatcaa agtgggacgt tttgggctcg tgccgaattc 1490

<210> 2  
<211> 756  
<212> DNA

3/88

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout Ten M3 coding sequence of carboxy termini of Ten M3

<400> 2  
 tccatctcgg ggggtgcaaca ggaagtgacc cggcaagcca aggcctttcct gtccttcgag 60  
 aggatgccgg agatccagct gagccgccgg cgctccaacc gggagaaacc ctggctgtgg 120  
 ttcgccaccg ccaagtctct gatcggtaag ggtgtcatgt tggcggtgac gcagggccgt 180  
 gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggctcg cgccgtcctc 240  
 aacaatgcgt tctacctgga ggacctgcac ttacagggtg agggacgcga cacgcactac 300  
 ttcatcaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg 360  
 aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tggatgaacgg 420  
 cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgct ccacgtgcgc 480  
 tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg 540  
 ttgtcgagtg cctgggtccag ggagcaacaa cgggtgaggg agggggagga gggggtgagg 600  
 ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac 660  
 gggactacg tcctctccat agagcagtac cccgagctag cagactccgc taacaacatc 720  
 cagttcctca ggcagagcga aataggggaag aggtaa 756

&lt;210&gt; 3

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout Ten M3 carboxy termini of Ten M3

&lt;400&gt; 3

Ser Ile Ser Gly Val Gln Gln Glu Val Thr Arg Gln Ala Lys Ala Phe  
 1 5 10 15

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser  
 20 25 30

4/88

Asn Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Ala Lys Ser Leu Ile  
 35 40 45

Gly Lys Gly Val Met Leu Ala Val Thr Gln Gly Arg Val Val Thr Asn  
 50 55 60

Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu  
 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly Arg  
 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu Gly  
 100 105 110

Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val Asn  
 115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg  
 130 135 140

Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val Arg  
 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln Ala  
 165 170 175

Arg Gln Lys Ala Leu Ser Ser Ala Trp Ser Arg Glu Gln Gln Arg Val  
 180 185 190

Arg Glu Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys Arg  
 195 200 205

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
 210 215 220

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
 225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
 245 250

&lt;210&gt; 4

5/88

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse Ten M1

&lt;400&gt; 4

Met Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe  
1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Gln Tyr Asn Glu Gly Arg  
20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val  
35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Glu Gly Ile Val Thr Ala  
50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile  
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly  
85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu  
100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val  
115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg  
130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile  
145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Met  
165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Gln Glu Gln Arg Arg

6/88

180	185	190
Leu Gln Glu Gly Glu Glu Gly Thr Arg Val Trp Thr Glu Gly Glu Lys		
195	200	205
Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe		
210	215	220
Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn		
225	230	235 240
Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg		
	245	250

<210> 5

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M2

<400> 5

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe	
1 5 10 15	
Leu Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile	
20 25 30	
Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly	
35 40 45	
Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val	
50 55 60	
Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn	
65 70 75 80	
Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp	
85 90 95	

7/88

Thr His Tyr Phe Val Lys Ile Gly Ala Ala Asp Gly Asp Leu Val Thr  
 100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val  
 115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe  
 130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr  
 145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp  
 165 170 175

Gln Ala Gly Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln  
 180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu  
 195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr  
 210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser  
 225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
 245 250

<210> 6

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M3

<400> 6

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe  
 1 5 10 15

8/88

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Lys Ala  
 20 25 30

Gly Ala Glu Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile  
 35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn  
 50 55 60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu  
 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys  
 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly  
 100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn  
 115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg  
 130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg  
 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala  
 165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val  
 180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg  
 195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
 210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
 225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
 245 250



9/88

&lt;210&gt; 7

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse Ten M4

&lt;400&gt; 7

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe  
 1 5 10 15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser  
 20 25 30

Cys Gln Gln Ala Pro Glu Thr Lys Lys Phe Ala Ser Ser Gly Ser Ile  
 35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr  
 50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Ile Ala Ala Ile  
 65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly  
 85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu  
 100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val  
 115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Met Leu Ile Gln Leu Gln Tyr  
 130 135 140

Arg Ala Leu Cys Leu Asn Thr Arg Tyr Gly Thr Thr Val Asp Glu Glu  
 145 150 155 160

Lys Val Arg Val Leu Glu Leu Ala Arg Gln Arg Ala Val Arg Gln Ala

10/88

	165		170		175										
Trp	Ala	Arg	Glu	Gln	Gln	Arg	Leu	Arg	Glu	Gly	Glu	Glu	Gly	Leu	Arg
	180						185						190		
Ala	Trp	Thr	Asp	Gly	Glu	Lys	Gln	Gln	Val	Leu	Asn	Thr	Gly	Arg	Val
	195						200					205			
Gln	Gly	Tyr	Asp	Gly	Phe	Phe	Val	Thr	Ser	Val	Glu	Gln	Tyr	Pro	Glu
	210						215				220				
Leu	Ser	Asp	Ser	Ala	Asn	Asn	Ile	His	Phe	Met	Arg	Gln	Ser	Glu	Met
	225				230					235					240
Gly Arg Arg															
<210> 8															
<211> 252															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Human Ten M1															
<400> 8															
Thr	Ile	Leu	Gly	Ile	Gln	Cys	Glu	Leu	Gln	Lys	Gln	Leu	Arg	Asn	Phe
1				5					10					15	
Ile	Ser	Leu	Asp	Gln	Leu	Pro	Met	Thr	Pro	Arg	Tyr	Asn	Asp	Gly	Arg
			20					25					30		
Cys	Leu	Glu	Gly	Gly	Lys	Gln	Pro	Arg	Phe	Ala	Ala	Val	Pro	Ser	Val
		35					40					45			
Phe	Gly	Lys	Gly	Ile	Lys	Phe	Ala	Ile	Lys	Asp	Gly	Ile	Val	Thr	Ala
	50					55					60				
Asp	Ile	Ile	Gly	Val	Ala	Asn	Glu	Asp	Ser	Arg	Arg	Leu	Ala	Ala	Ile
65					70					75					80

11/88

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly  
                             85                            90                            95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu  
                             100                            105                            110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val  
                             115                            120                            125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg  
                             130                            135                            140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile  
                             145                            150                            155                            160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile  
                             165                            170                            175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg  
                             180                            185                            190

Leu Gln Glu Gly Glu Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys  
                             195                            200                            205

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
                             210                            215                            220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
                             225                            230                            235                            240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
                             245                            250

&lt;210&gt; 9

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human Ten M2

&lt;400&gt; 9

12/88

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe  
 1 5 10 15  
 Met Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile  
 20 25 30  
 Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly  
 35 40 45  
 Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val  
 50 55 60  
 Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn  
 65 70 75 80  
 Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp  
 85 90 95  
 Thr His Tyr Phe Val Lys Ile Gly Ser Ala Asp Gly Asp Leu Val Thr  
 100 105 110  
 Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val  
 115 120 125  
 Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe  
 130 135 140  
 Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr  
 145 150 155 160  
 Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp  
 165 170 175  
 Gln Ala Arg Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln  
 180 185 190  
 Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu  
 195 200 205  
 Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr  
 210 215 220  
 Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser  
 225 230 235 240

13/88

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
 245 250

<210> 10

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Ten M3

<400> 10

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe  
 1 5 10 15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Arg Ala  
 20 25 30

Gly Gly Ala Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile  
 35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn  
 50 55 60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu  
 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys  
 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly  
 100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn  
 115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg  
 130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg

14/88

145					150					155					160
Tyr	Gly	Met	Thr	Leu	Asp	Glu	Glu	Lys	Ala	Arg	Ile	Leu	Glu	Gln	Ala
				165					170					175	
Arg	Gln	Arg	Ala	Leu	Ala	Arg	Ala	Trp	Ala	Arg	Glu	Gln	Gln	Arg	Val
			180					185					190		
Arg	Asp	Gly	Glu	Glu	Gly	Ala	Arg	Leu	Trp	Thr	Glu	Gly	Glu	Lys	Arg
		195					200					205			
Gln	Leu	Leu	Ser	Ala	Gly	Lys	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Tyr	Val
	210					215					220				
Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn	Ile
225					230					235					240
Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile	Gly	Arg	Arg					
				245					250						
<210> 11															
<211> 252															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Human Ten M4															
<400> 11															
Ser	Ile	Leu	Gly	Val	Gln	Cys	Glu	Val	Gln	Lys	Gln	Leu	Lys	Ala	Phe
1				5					10					15	
Val	Thr	Leu	Glu	Arg	Phe	Asp	Gln	Leu	Tyr	Gly	Ser	Thr	Ile	Thr	Ser
			20					25					30		
Cys	Leu	Gln	Ala	Pro	Lys	Thr	Lys	Lys	Phe	Ala	Ser	Ser	Gly	Ser	Val
		35					40					45			
Phe	Gly	Lys	Gly	Val	Lys	Phe	Ala	Leu	Lys	Asp	Gly	Arg	Val	Thr	Thr
	50					55					60				

15/88

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Val Ala Ala Ile  
 65 70 75 80  
 Leu Asn His Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly  
 85 90 95  
 Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu  
 100 105 110  
 Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val  
 115 120 125  
 Asn Val Thr Val Ser Gln Ile Asn Thr Val Leu Ser Gly Arg Thr Arg  
 130 135 140  
 Arg Tyr Thr Asp Ile Gln Leu Gln Tyr Gly Ala Leu Cys Leu Asn Thr  
 145 150 155 160  
 Arg Tyr Gly Thr Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Leu  
 165 170 175  
 Ala Arg Gln Arg Ala Val Arg Gln Ala Trp Ala Arg Glu Gln Gln Arg  
 180 185 190  
 Leu Arg Glu Gly Glu Glu Gly Leu Arg Ala Trp Thr Glu Gly Glu Lys  
 195 200 205  
 Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
 210 215 220  
 Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
 225 230 235 240  
 Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
 245 250

&lt;210&gt; 12

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

16/88

&lt;223&gt; Zebrafish Ten M3

&lt;400&gt; 12

Ser Ile Ser Gly Val Gln Gln Glu Val Met Arg Gln Ala Lys Ala Phe  
 1 5 10 15

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser  
 20 25 30

Ser Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile  
 35 40 45

Gly Lys Gly Val Met Leu Ala Ile Thr Ser Lys Gly Gln Val Ala Thr  
 50 55 60

Asn Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Val Thr Val  
 65 70 75 80

Leu Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly  
 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu  
 100 105 110

Gly Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val  
 115 120 125

Asn Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg  
 130 135 140

Arg Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val  
 145 150 155 160

Arg Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln  
 165 170 175

Ala Arg Gln Arg Ala Leu Ser Ser Ala Trp Ala Arg Glu Gln Gln Arg  
 180 185 190

Val Arg Asp Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys  
 195 200 205

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
 210 215 220



17/88

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
 225 230 235 240

Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
 245 250

&lt;210&gt; 13

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout TCAP3 (40a.a.)

&lt;400&gt; 13

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
 1 5 10 15

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
 20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile  
 35 40

&lt;210&gt; 14

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout TCAP 3 (41a.a.)

&lt;400&gt; 14

Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
 1 5 10 15

Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn

18/88

20

25

30

Ile Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

&lt;210&gt; 15

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout preTCAP3 (43 a.a.)

&lt;400&gt; 15

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
35 40

&lt;210&gt; 16

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout preTCAP3 (44 a.a.)

&lt;400&gt; 16

Arg Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

19/88

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
 35 40

&lt;210&gt; 17

&lt;211&gt; 120

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout TCAP3 (120 n.a.)

<400> 17  
 cagctgctga gcgggaggaa gggtctgggc tacgacgggt actacgtcct ctccatagag 60  
 cagtaccccc agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata 120

&lt;210&gt; 18

&lt;211&gt; 123

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout TCAP3 (123 n.a.)

<400> 18  
 aggcagctgc tgagcgggag gaagggtctg ggctacgacg ggtactacgt cctctccata 60  
 gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa 120  
 ata 123

&lt;210&gt; 19

&lt;211&gt; 129

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rainbow Trout preTCAP3 (129 n.a.)

20/88

<400> 19  
 cagctgctga gcgggaggaa ggttctgggc tacgacgggt actacgtcct ctccatagag 60  
 cagtacccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata 120  
 gggaagagg 129

<210> 20

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (132 n.a.)

<400> 20  
 aggcagctgc tgagcgggag gaaggttctg ggctacgacg ggtactacgt cctctccata 60  
 gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa 120  
 atagggaaga gg 132

<210> 21

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (40 a.a.)

<400> 21

Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
 1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val  
 20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile  
 35 40

21/88

&lt;210&gt; 22

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Zebrafish TCAP3 (41 a.a.)

&lt;400&gt; 22

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Val Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

&lt;210&gt; 23

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Zebrafish preTCAP3 (43 a.a.)

&lt;400&gt; 23

Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
35 40

&lt;210&gt; 24

&lt;211&gt; 44

22/88

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP3 (44 a.a.)

<400> 24

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg  
35 40

<210> 25

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (120 n.a.)

```
<400> 25
cagttgctca gctctgggaa ggtgctgggt tacgatgggt actatgtact atcagtgagg 60
caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata 120
```

<210> 26

<211> 123

<212> DNA

<213> Artificial Sequence

**<220>**

<223> Zebrafish TCAP3 (123 n.a.)

23/88

<400> 26  
 aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg 60  
 gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag 120  
 ata 123

<210> 27

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP3 (129 n.a.)

<400> 27  
 cagttgctca gctctgggaa ggtgctgggt tacgatgggt actatgtact atcagtggag 60  
 caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata 120  
 gggaagagg 129

<210> 28

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP3 (132 n.a.)

<400> 28  
 aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg 60  
 gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag 120  
 ataggaaga gg 132

<210> 29

<211> 40

<212> PRT

<213> Artificial Sequence

24/88

&lt;220&gt;

&lt;223&gt; Zebrafish TCAP4 (40 a.a.)

&lt;400&gt; 29

Gln	Leu	Leu	Ser	Ser	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Phe	Tyr	Ile
1				5					10					15	

Val	Ser	Val	Asp	Gln	Phe	Pro	Glu	Leu	Thr	Asp	Asn	Ile	Asn	Asn	Val
			20					25					30		

His	Phe	Trp	Arg	Gln	Thr	Glu	Met
		35					40

&lt;210&gt; 30

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Zebrafish TCAP4 (41 a.a.)

&lt;400&gt; 30

Gln	Gln	Leu	Leu	Ser	Ser	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Phe	Tyr
1				5					10					15	

Ile	Val	Ser	Val	Asp	Gln	Phe	Pro	Glu	Leu	Thr	Asp	Asn	Ile	Asn	Asn
			20					25					30		

Val	His	Phe	Trp	Arg	Gln	Thr	Glu	Met
		35						40

&lt;210&gt; 31

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



25/88

&lt;220&gt;

&lt;223&gt; Zebrafish preTCAP4 (43 a.a.)

&lt;400&gt; 31

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile  
1 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val  
20 25 30

His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg  
35 40

&lt;210&gt; 32

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Zebrafish preTCAP4 (44 a.a.)

&lt;400&gt; 32

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr  
1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn  
20 25 30

Val His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg  
35 40

&lt;210&gt; 33

&lt;211&gt; 120

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Zebrafish TCAP4 (120 n.a.)

26/88

<400> 33  
cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60  
cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120

<210> 34

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP4 (123 n.a.)

<400> 34  
cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc 60  
gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120  
atg 123

<210> 35

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP4 (129 n.a.)

<400> 35  
cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60  
cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120  
ggacgcagg 129

<210> 36

<211> 132

<212> DNA

<213> Artificial Sequence

27/88

&lt;220&gt;

&lt;223&gt; Zebrafish preTCAP4 (132 n.a.)

<400> 36  
cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc 60  
gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120  
atggggacgca gg 132

&lt;210&gt; 37

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP1 (40 a.a.)

&lt;400&gt; 37

Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
20 25 30

His Phe Met Arg Gln Ser Glu Ile  
35 40

&lt;210&gt; 38

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP1 (41 a.a.)

&lt;400&gt; 38

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe

28/88

1					5					10					15
Val	Leu	Ser	Val	Glu	Gln	Tyr	Leu	Glu	Leu	Ser	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile His Phe Met Arg Gln Ser Glu Ile  
35 40

<210> 39 .

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (43 a.a.)

<400> 39

Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
20 25 30

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
35 40

<210> 40

<211> 44

<212> PRT

<213> Artificial Sequence

**<220>**

<223> Mouse preTCAP1 (44 a.a.)

<400> 40

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
1 5 10 15

29/88

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
                   20                  25                  30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
           35                  40

&lt;210&gt; 41

&lt;211&gt; 120

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP1 (120 n.a.)

<400> 41  
 cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60  
 cagtatttag aactttcaga cagtgcacaac aatattcact tcatgagaca gagtgaata 120

&lt;210&gt; 42

&lt;211&gt; 123

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP1 (123 n.a.)

<400> 42  
 cagcagcttt tgggcaccgg gaggggtgcag gggatatgatg ggtattttgt cttgtctgtt 60  
 gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa 120  
 ata 123

&lt;210&gt; 43

&lt;211&gt; 129

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

30/88

&lt;220&gt;

&lt;223&gt; Mouse preTCAP1 (129 n.a.)

<400> 43  
 cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60  
 cagtatttag aactttcaga cagtgcacaac aatattcact tcatgagaca gagtgaaata 120  
 ggcaggagg 129

&lt;210&gt; 44

&lt;211&gt; 132

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP1 (132 n.a.)

<400> 44  
 cagcagcttt tgggcaccgg gaggggtgcag gggatatgatg ggtattttgt cttgtctgtt 60  
 gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa 120  
 ataggcagga gg 132

&lt;210&gt; 45

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP2 (40 a.a.)

&lt;400&gt; 45

Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr	Val
1				5				10						15	

Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn	Ile
			20				25						30		

31/88

Gln Phe Leu Arg Gln Asn Glu Ile  
35 40

&lt;210&gt; 46

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP2 (41 a.a.)

&lt;400&gt; 46

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr  
1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn  
20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met  
35 40

&lt;210&gt; 47

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP2 (43 a.a)

&lt;400&gt; 47

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val  
1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile  
20 25 30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg  
35 40

32/88

&lt;210&gt; 48

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP2 (44 a.a.)

&lt;400&gt; 48

Gln	Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Asn	Glu	Met	Gly	Lys	Arg
		35					40				

&lt;210&gt; 49

&lt;211&gt; 120

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP2 (120 n.a.)

<400> 49	
caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa	60
cagtaccccg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagagg	120

&lt;210&gt; 50

&lt;211&gt; 123

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



33/88

&lt;220&gt;

&lt;223&gt; Mouse TCAP 2 (123 n.a.)

<400> 50  
cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60  
gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120  
atg 123

&lt;210&gt; 51

&lt;211&gt; 129

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP2 (129 n.a.)

<400> 51  
caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa 60  
cagtaccgga agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagatg 120  
ggaaagagg 129

&lt;210&gt; 52

&lt;211&gt; 132

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP2 (132 n.a.)

<400> 52  
cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60  
gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120  
atgggaaaga gg 132

&lt;210&gt; 53

&lt;211&gt; 40

34/88

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP3 (40 a.a.)

&lt;400&gt; 53

Gln	Leu	Leu	Ser	Ala	Gly	Lys	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Tyr	Val
1				5					10					15	

Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn	Ile
			20					25					30		

Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile
		35				40	

&lt;210&gt; 54

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP3 (41 a..a)

&lt;400&gt; 54

Arg	Gln	Leu	Leu	Ser	Ala	Gly	Lys	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile
		35				40		

&lt;210&gt; 55

&lt;211&gt; 43

&lt;212&gt; PRT

35/88

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP3 (43 a.a.)

&lt;400&gt; 55

Gln	Leu	Leu	Ser	Ala	Gly	Lys	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Tyr	Val
1				5					10					15	

Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn	Ile
			20					25					30		

Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile	Gly	Lys	Arg
		35					40			

&lt;210&gt; 56

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP3 (44 a.a.)

&lt;400&gt; 56

Arg	Gln	Leu	Leu	Ser	Ala	Gly	Lys	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile	Gly	Lys	Arg
		35					40				

&lt;210&gt; 57

&lt;211&gt; 120

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

36/88

&lt;220&gt;

&lt;223&gt; Mouse TCAP3 (120 n.a.)

<400> 57  
cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag 60  
cagtacccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc 120

&lt;210&gt; 58

&lt;211&gt; 123

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP3 (123 n.a.)

<400> 58  
cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcgggtg 60  
gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag 120  
atc 123

&lt;210&gt; 59

&lt;211&gt; 129

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP3 (129 n.a.)

<400> 59  
cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag 60  
cagtacccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc 120  
ggcaagagg 129

&lt;210&gt; 60

&lt;211&gt; 132

37/88

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP3 (132 n.a.)

<400> 60  
 cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcgggtg 60  
 gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag 120  
 atcggcaaga gg 132

&lt;210&gt; 61

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP4 (40 a.a.)

&lt;400&gt; 61

Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val  
 1 5 10 15  
 Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile  
 20 25 30  
 His Phe Met Arg Gln Ser Glu Met  
 35 40

&lt;210&gt; 62

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse TCAP4 (41 a.a.)

38/88

&lt;400&gt; 62

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
1 5 10 15

Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
20 25 30

Ile His Phe Met Arg Gln Ser Glu Met  
35 40

&lt;210&gt; 63

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP4 (43 a.a.)

&lt;400&gt; 63

Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val  
1 5 10 15

Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile  
20 25 30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
35 40

&lt;210&gt; 64

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP4 (44 a.a.)

&lt;400&gt; 64

39/88

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
 1 5 10 15

Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
 35 40

<210> 65

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP4 (120 n.a.)

<400> 65  
 caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggctcgag 60  
 cagtacccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120

<210> 66

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse TCAP4 (123 n.a.)

<400> 66  
 cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc 60  
 gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag 120  
 atg 123

<210> 67

<211> 129

<212> DNA

40/88

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP4 (129 n.a.)

<400> 67  
 caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag 60  
 cagtaccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120  
 ggccgaagg 129

&lt;210&gt; 68

&lt;211&gt; 132

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mouse preTCAP4 (132 n.a.)

<400> 68  
 cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc 60  
 gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag 120  
 atggggccgaa gg 132

&lt;210&gt; 69

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP1 (40 a.a.)

&lt;400&gt; 69

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
 1 5 10 15



41/88

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
20 25 30

His Phe Met Arg Gln Ser Glu Ile  
35 40

&lt;210&gt; 70

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP1 (41 a.a.)

&lt;400&gt; 70

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile  
35 40

&lt;210&gt; 71

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP1 (43 a.a.)

&lt;400&gt; 71

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile  
20 25 30

42/88

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
           35                          40

&lt;210&gt; 72

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP1 (44 a.a.)

&lt;400&gt; 72

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
   1                  5                  10                  15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
           20                  25                  30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg  
           35                          40

&lt;210&gt; 73

&lt;211&gt; 120

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP1 (120 n.a.)

<400> 73  
 cagcttttga gcactgggcg ggtacaaggt tacgatgggt attttggttt gtctgttgag 60  
 cagtatttag aactttctga cagtgcgaat aatattcact ttatgagaca gagcgaaata 120

&lt;210&gt; 74

&lt;211&gt; 123

&lt;212&gt; DNA

43/88

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP1 (123 n.a.)

<400> 74  
 cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtatattgt tttgtctgtt 60  
 gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa 120  
 ata 123

&lt;210&gt; 75

&lt;211&gt; 129

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP1 (129 n.a.)

<400> 75  
 cagcttttga gcactgggcy ggtacaaggt tacgatgggt attttgtttt gtctgttgag 60  
 cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata 120  
 ggcaggagg 129

&lt;210&gt; 76

&lt;211&gt; 132

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP1 (132 n.a.)

<400> 76  
 cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtatattgt tttgtctgtt 60  
 gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa 120  
 ataggcagga gg 132

44/88

&lt;210&gt; 77

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP2 (40 a.a.)

&lt;400&gt; 77

Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr	Val
1				5					10					15	

Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn	Ile
			20					25					30		

Gln	Phe	Leu	Arg	Gln	Asn	Glu	Met
		35					40

&lt;210&gt; 78

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP2 (41 a.a.)

&lt;400&gt; 78

Gln	Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr
1				5						10				15	

Val	Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Asn	Glu	Met
		35						40

&lt;210&gt; 79

45/88

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP2 (43 a.a.)

&lt;400&gt; 79

Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr	Val
1				5				10						15	

Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn	Ile
			20					25					30		

Gln	Phe	Leu	Arg	Gln	Asn	Glu	Met	Gly	Lys	Arg
		35					40			

&lt;210&gt; 80

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP2 (44 a.a.)

&lt;400&gt; 80

Gln	Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Asn	Glu	Met	Gly	Lys	Arg
		35					40				

&lt;210&gt; 81

&lt;211&gt; 120

&lt;212&gt; DNA

46/88

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP2 (120 n.a.)

<400> 81  
cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag 60  
caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg 120

&lt;210&gt; 82

&lt;211&gt; 123

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP2 (123 n.a.)

<400> 82  
cagcagcttc tgagcaccgg gcgcgtgcaa gggtacgagg gatattacgt gcttcccgtg 60  
gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag 120  
atg 123

&lt;210&gt; 83

&lt;211&gt; 129

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP2 (129 n.a.)

<400> 83  
cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag 60  
caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg 120  
ggaaagagg 129

47/88

&lt;210&gt; 84

&lt;211&gt; 132

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP2 (132 n.a.)

<400> 84  
 cagcagcttc tgagcaccgg gcgcgtgcaa gggtagcagg gatattacgt gcttcccggtg 60  
 gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag 120  
 atgggaaaga gg 132

&lt;210&gt; 85

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP3 (40 a.a.)

&lt;400&gt; 85

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
 1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
 20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile  
 35 40

&lt;210&gt; 86

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

48/88

&lt;220&gt;

&lt;223&gt; Human TCAP3 (41 a.a.)

&lt;400&gt; 86

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr  
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn  
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile  
35 40

&lt;210&gt; 87

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP3 (43 a.a.)

&lt;400&gt; 87

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val  
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile  
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg  
35 40

&lt;210&gt; 88

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;



49/88

&lt;223&gt; Human preTCAP3 (44 a.a.)

&lt;400&gt; 88

Arg	Gln	Leu	Leu	Ser	Ala	Gly	Lys	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Ser	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile	Gly	Arg	Arg
			35				40				

&lt;210&gt; 89

&lt;211&gt; 120

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP3 (120 n.a.)

<400> 89	
cagctgctga ggcgcggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag	60
cagtaccccg agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc	120

&lt;210&gt; 90

&lt;211&gt; 123

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP3 (123 n.a.)

<400> 90	
cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggtg	60
gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag	120
atc	123

&lt;210&gt; 91

50/88

&lt;211&gt; 129

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP (129 n.a.)

<400> 91  
cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag 60  
cagtacccccg agctggccga cagcgccaac aacatccagt tcctgcgga gagcgagatc 120  
ggcaggagg 129

&lt;210&gt; 92

&lt;211&gt; 132

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP3 (132 n.a.)

<400> 92  
cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcgggtg 60  
gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag 120  
atcggcagga gg 132

&lt;210&gt; 93

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP4 (40 a.a.)

&lt;400&gt; 93

51/88

Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val  
 1 5 10 15

Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile  
 20 25 30

His Phe Met Arg Gln Ser Glu Met  
 35 40

&lt;210&gt; 94

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP4 (41 a.a.)

&lt;400&gt; 94

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
 1 5 10 15

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Met  
 35 40

&lt;210&gt; 95

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP4 (43 a..a)

&lt;400&gt; 95

Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val  
 1 5 10 15

52/88

Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile  
                   20                  25                  30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
                   35                  40

&lt;210&gt; 96

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP4 (44 a.a.)

&lt;400&gt; 96

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe  
   1                  5                  10                  15

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn  
                   20                  25                  30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg  
                   35                  40

&lt;210&gt; 97

&lt;211&gt; 120

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP4 (120 n.a.)

<400> 97  
 caggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag 60  
 cagtacccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg 120

&lt;210&gt; 98

53/88

&lt;211&gt; 123

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human TCAP4 (123 n.a.)

<400> 98  
cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc 60  
gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag 120  
atg 123

&lt;210&gt; 99

&lt;211&gt; 129

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP4 (129 n.a.)

<400> 99  
caggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag 60  
cagtaccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg 120  
ggccggagg 129

&lt;210&gt; 100

&lt;211&gt; 132

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human preTCAP4 (132 n.a.)

<400> 100  
cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc 60

54/88

gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag 120  
 atggggccgga gg 132

&lt;210&gt; 101

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; G. gallus TCAP-1

&lt;400&gt; 101

Gln Gln Leu Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe  
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn  
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile  
 35 40

&lt;210&gt; 102

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Zebrafish TCAP-4

&lt;400&gt; 102

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr  
 1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn  
 20 25 30

Val His Phe Trp Arg Gln Thr Glu Met  
 35 40

55/88

&lt;210&gt; 103

&lt;211&gt; 37

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; D. melanogaster Ten-m gene product

&lt;400&gt; 103

Glu Leu Val Gln His Gly Asp Val Asp Gly Trp Asn Gly Asp Ile His  
1 5 10 15

Ser Ile His Lys Tyr Pro Gln Leu Ala Asp Pro Gly Asn Val Ala Phe  
20 25 30

Gln Arg Asp Ala Lys  
35

&lt;210&gt; 104

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human CRF TCAP like region

&lt;400&gt; 104

Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg  
1 5 10 15

Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His  
20 25 30

Ser Asn Arg Lys Leu Met Glu Ile Ile  
35 40

&lt;210&gt; 105

56/88

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human urocortin TCAP-like region

&lt;400&gt; 105

Asp Asn Pro Ser Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr  
1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln  
20 25 30

Asn Arg Ile Ile Phe Asp Ser Val  
35 40

&lt;210&gt; 106

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human urocortin 2 TCAP-like region

&lt;400&gt; 106

Ile Val Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Gln Ile Leu Leu  
1 5 10 15

Glu Gln Ala Arg Ala Arg Ala Ala Arg Glu Gln Ala Thr Thr Asn Ala  
20 25 30

Arg Ile Leu Ala Arg Val  
35

&lt;210&gt; 107

&lt;211&gt; 38



57/88

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human urocortin 3 TCAP=like region

&lt;400&gt; 107

Phe	Thr	Leu	Ser	Leu	Asp	Val	Pro	Thr	Asn	Ile	Met	Asn	Leu	Leu	Phe
1				5					10					15	

Asn	Ile	Ala	Lys	Ala	Lys	Asn	Leu	Arg	Ala	Gln	Ala	Ala	Ala	Asn	Ala
			20					25					30		

His	Leu	Met	Ala	Gln	Ile
		35			

&lt;210&gt; 108

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; L. migratoria DP

&lt;400&gt; 108

Met	Gly	Met	Gly	Pro	Ser	Leu	Ser	Ile	Val	Asn	Pro	Met	Asp	Val	Leu
1				5					10					15	

Arg	Gln	Arg	Leu	Leu	Leu	Glu	Ile	Ala	Arg	Arg	Arg	Leu	Arg	Asp	Ala
			20					25					30		

Glu	Glu	Gln	Ile	Lys	Ala	Asn	Lys	Asp	Phe	Leu	Gln	Gln	Ile
		35					40					45	

&lt;210&gt; 109

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

58/88

&lt;220&gt;

&lt;223&gt; A. domesticus DP

&lt;400&gt; 109

Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg  
1 5 10 15

Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln  
20 25 30

Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile  
35 40 45

&lt;210&gt; 110

&lt;211&gt; 39

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; T. molitor DP

&lt;400&gt; 110

Ser Pro Thr Ile Ser Ile Thr Ala Pro Ile Asp Val Leu Arg Lys Thr  
1 5 10 15

Trp Glu Gln Glu Arg Ala Arg Lys Gln Met Val Ala Gln Asn Asn Arg  
20 25 30

Glu Phe Leu Asn Ser Leu Asn  
35

&lt;210&gt; 111

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

59/88

&lt;220&gt;

&lt;223&gt; M. sexta DP-1

&lt;400&gt; 111

Arg Met Pro Ser Leu Ser Ile Asp Leu Pro Met Ser Val Leu Arg Gln  
 1 5 10 15

Lys Leu Ser Leu Glu Lys Glu Arg Lys Val His Ala Leu Arg Ala Ala  
 20 25 30

Ala Asn Arg Asn Phe Leu Asn Asp Ile  
 35 40

&lt;210&gt; 112

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; M. sexta DP-II

&lt;400&gt; 112

Ser Leu Ser Val Asn Pro Ala Val Asp Ile Leu Gln His Arg Tyr Met  
 1 5 10 15

Glu Lys Val Ala Gln Asn Asn Arg Asn Phe Leu Asn Arg Val  
 20 25 30

&lt;210&gt; 113

&lt;211&gt; 45

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P. Americana

&lt;400&gt; 113

Thr Gly Ser Gly Pro Ser Leu Ser Ile Val Asn Pro Leu Asp Val Leu

60/88

1                      5                      10                      15  
Arg Gln Arg Leu Leu Leu Glu Ile Ala Arg Arg Arg Met Arg Gln Ser  
20                      25                      30

Gln Asp Gln Ile Gln Asn Arg Glu Ile Leu Gln Thr Ile  
35 40 45

<210> 114

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> O. keta CRP

<400> 114

Ser Asp Asp Pro Pro Ile Ser Leu Asp Leu Thr Phe His Met Leu Arg  
1 5 10 15

Gln Met Asn Glu Met Ser Arg Ala Glu Gln Leu Gln Gln Gln Ala His  
20 25 30

Ser Asn Arg Lys Met Met Glu Ile Phe  
35 40

<210> 115

<211> 40

<212> PRT

<213> Artificial Sequence

**<220>**

<223> R. norvegicus

<400> 115

Asp Asp Pro Pro Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr  
1 5 10 15

61/88

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln  
20 25 30

Asn Arg Ile Ile Phe Asp Ser Val  
35 40

&lt;210&gt; 116

&lt;211&gt; 37

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P. sauvageii

&lt;400&gt; 116

Gln Gly Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys  
1 5 10 15

Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn  
20 25 30

Asn Arg Leu Leu Leu  
35

&lt;210&gt; 117

&lt;211&gt; 41

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; C. carpio US

&lt;400&gt; 117

Asn Asp Asp Pro Pro Ile Ser Ile Asp Leu Thr Phe His Leu Leu Arg  
1 5 10 15

Asn Met Ile Glu Met Ala Arg Asn Glu Asn Gln Arg Glu Gln Ala Gly  
20 25 30

62/88

Leu Asn Arg Lys Tyr Leu Asp Glu Val  
35 40

&lt;210&gt; 118

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; M. Musculus UCN2

&lt;400&gt; 118

Val Ile Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Arg Ile Leu Leu  
1 5 10 15

Glu Gln Ala Arg Tyr Lys Ala Ala Arg Asn Gln Ala Ala Thr Asn Ala  
20 25 30

Gln Ile Leu Ala His Val  
35

&lt;210&gt; 119

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; R. dano UCN2

&lt;400&gt; 119

Leu Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Val Leu Phe  
1 5 10 15

Asp Val Ala Lys Ala Lys Asn Leu Arg Ala Lys Ala Ala Glu Asn Ala  
20 25 30

Arg Leu Leu Ala His Ile  
35

63/88

&lt;210&gt; 120

&lt;211&gt; 305

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Hamster 305bp urocortin cDNA probe examples "cloning mRNA"

<400> 120  
attcaccgcc gctcgggatc tgagcctgca ggcgagcggc agcgacggga agaccttccg 60  
ctgtccatcg acctcacatt ccacctgcta cggaccctgc tggagatggc ccggacacag 120  
agccaacgcg agcgagcaga gcagaaccga atcataactca acgcggtggg caagtgatcg 180  
gcccgggtgtg ggaccccaaa aggctcgacc ctttccccta cctaccccgg ggctgaagtc 240  
acgcgaccga agtcggctta gtcccgcggt gcagcgcctc ccagagttac cctgaacaat 300  
cccgc 305

&lt;210&gt; 121

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TCAP1 fwd primer

<400> 121  
acgtcagtgt tgatgggagg acta 24

&lt;210&gt; 122

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

64/88

&lt;223&gt; TCAP1 rvs primer

&lt;400&gt; 122

cctcctgcct atttcactct gtctcat

27

&lt;210&gt; 123

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TCAP2 Fwd primer

&lt;400&gt; 123

tcgagggcaa ggacacacac tactt

25

&lt;210&gt; 124

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TCAP2 rvs primer

&lt;400&gt; 124

aagaactgga tgttgctgct actgtc

26

&lt;210&gt; 125

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TCAP3 fwd primer

&lt;400&gt; 125

caacaacgcc ttctacctgg agaac

25



65/88

&lt;210&gt; 126

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TCAP3 rvs primer

&lt;400&gt; 126

tggtgtggc actgtcagcc a

21

&lt;210&gt; 127

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TCAP4 fwd primer

&lt;400&gt; 127

tttgctcca gtggttccat ctt

23

&lt;210&gt; 128

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TCAP4 rvs primer

&lt;400&gt; 128

tggatattgt tggcgctgtc tgac

24

&lt;210&gt; 129

&lt;211&gt; 6

66/88

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Conserved motif between CRF and TCAP I/L S X X (X)-L/V at amino  
terminus

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (1) .. (1)

&lt;223&gt; X=I or L

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (3) .. (3)

&lt;223&gt; X=T or A

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (4) .. (4)

&lt;223&gt; X=L, I or G

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (5) .. (5)

&lt;223&gt; X=D, R or K

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (6) .. (6)

&lt;223&gt; X=L or V

67/88

&lt;400&gt; 129

Xaa Ser Xaa Xaa Xaa Xaa  
1 5

&lt;210&gt; 130

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Conserved motif between CRF and TCAP - In middle L/V-L/I-X-V/aliphatic residue

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (1)..(1)

&lt;223&gt; X=V or L

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (4)..(4)

&lt;223&gt; X=M, L Q, I or V

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (2)..(2)

&lt;223&gt; X=L, I or F

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (3)..(3)

68/88

<223> X=E, N, S or P

<400> 130

Xaa Xaa Xaa Xaa  
1

<210> 131

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Conserved motif between CRF and TCAP N/I/A-H/basic residue -I/L/F  
/-aliphatic at carboxy terminus

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> X=R, A or I

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> X=H or basic residues, K, I, R or Q

<220>

<221> MISC\_FEATURE

<222> (4)..(4)

<223> X=I, L or F

<400> 131

Asn Xaa Xaa Xaa

69/88

1

&lt;210&gt; 132

&lt;211&gt; 8964

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (50)..(8197)

&lt;223&gt;

&lt;400&gt; 132

aagttctaag aagccggacc gatgtgcaca gagaaggaat gaaggaagt atg gat gtg 58  
 Met Asp Val  
 1

aag gaa cgc agg cct tac tgc tcc ttg acc aag agc aga cgg gaa aag 106  
 Lys Glu Arg Arg Pro Tyr Cys Ser Leu Thr Lys Ser Arg Arg Glu Lys  
 5 10 15

gaa agg cgc tat aca aat tgc tcc gcg gac aat gag gag tgt agg gtc 154  
 Glu Arg Arg Tyr Thr Asn Ser Ser Ala Asp Asn Glu Glu Cys Arg Val  
 20 25 30 35

ccc acg cag aag tcc tat agt tcc agt gaa acc ttg aaa gct ttc gat 202  
 Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala Phe Asp  
 40 45 50

cat gat tat tca cgg ctg ctt tat gga aac aga gta aag gat ttg gtc 250  
 His Asp Tyr Ser Arg Leu Leu Tyr Gly Asn Arg Val Lys Asp Leu Val  
 55 60 65

cac aga gaa gcc gac gag tat act aga caa gga cag aat ttt acc cta 298  
 His Arg Glu Ala Asp Glu Tyr Thr Arg Gln Gly Gln Asn Phe Thr Leu  
 70 75 80

agg cag tta gga gtg tgt gaa tcc gca act cga aga gga gtg gca ttc 346  
 Arg Gln Leu Gly Val Cys Glu Ser Ala Thr Arg Arg Gly Val Ala Phe  
 85 90 95

tgt gcg gaa atg ggg ctc cct cac aga ggt tac tcc atc agt gca ggg 394  
 Cys Ala Glu Met Gly Leu Pro His Arg Gly Tyr Ser Ile Ser Ala Gly  
 100 105 110 115

tca gat gcg gat acg gaa aac gaa gca gtg atg tcc cct gag cat gcc 442  
 Ser Asp Ala Asp Thr Glu Asn Glu Ala Val Met Ser Pro Glu His Ala  
 120 125 130

70/88

atg aga ctt tgg ggc agg ggg gtc aaa tcg ggc cgc agt tcc tgc ctg	490
Met Arg Leu Trp Gly Arg Gly Val Lys Ser Gly Arg Ser Ser Cys Leu	
135 140 145	
tca agc cgg tcc aac tcc gcc ctc acc ctg aca gac acg gag cac gag	538
Ser Ser Arg Ser Asn Ser Ala Leu Thr Leu Thr Asp Thr Glu His Glu	
150 155 160	
aac agg tcg gac agt gag agc gag caa cct tca aac aac cca ggg caa	586
Asn Arg Ser Asp Ser Glu Ser Glu Gln Pro Ser Asn Asn Pro Gly Gln	
165 170 175	
ccc acc ctg cag cct ttg ccg cca tcc cac aag cag cac ccg gcg cag	634
Pro Thr Leu Gln Pro Leu Pro Pro Ser His Lys Gln His Pro Ala Gln	
180 185 190 195	
cat cac ccg tcc atc act tcc ctc aat aga aac tcc ctg acc aat aga	682
His His Pro Ser Ile Thr Ser Leu Asn Arg Asn Ser Leu Thr Asn Arg	
200 205 210	
agg aac cag agt ccg gcc ccg ccg gct gct ttg ccc gcc gag ctg caa	730
Arg Asn Gln Ser Pro Ala Pro Pro Ala Ala Leu Pro Ala Glu Leu Gln	
215 220 225	
acc aca ccc gag tcc gtc cag ctg cag gac agc tgg gtc ctt ggc agt	778
Thr Thr Pro Glu Ser Val Gln Leu Gln Asp Ser Trp Val Leu Gly Ser	
230 235 240	
aat gta cca ctg gaa agc agg cat ttc cta ttc aaa aca ggg aca ggg	826
Asn Val Pro Leu Glu Ser Arg His Phe Leu Phe Lys Thr Gly Thr Gly	
245 250 255	
acg acg cca ctg ttc agt acg gca acc ccg gga tac aca atg gca tct	874
Thr Thr Pro Leu Phe Ser Thr Ala Thr Pro Gly Tyr Thr Met Ala Ser	
260 265 270 275	
ggc tct gtt tat tct ccg cct acc ccg cca ctt cct aga aac acc cta	922
Gly Ser Val Tyr Ser Pro Pro Thr Arg Pro Leu Pro Arg Asn Thr Leu	
280 285 290	
tca aga agt gct ttt aaa ttc aag aag tct tca aag tac tgc agc tgg	970
Ser Arg Ser Ala Phe Lys Phe Lys Lys Ser Ser Lys Tyr Cys Ser Trp	
295 300 305	
agg tgc acc gca ctg tgt gct gta ggg gtc tca gtg ctc ctg gcc att	1018
Arg Cys Thr Ala Leu Cys Ala Val Gly Val Ser Val Leu Leu Ala Ile	
310 315 320	
ctc ctc tcc tat ttt ata gca atg cat cta ttt ggc ctc aac tgg cac	1066
Leu Leu Ser Tyr Phe Ile Ala Met His Leu Phe Gly Leu Asn Trp His	
325 330 335	
tta cag cag acg gaa aat gac aca ttc gag aat gga aaa gtg aat tct	1114
Leu Gln Gln Thr Glu Asn Asp Thr Phe Glu Asn Gly Lys Val Asn Ser	
340 345 350 355	
gac acc gtg cca aca aac act gta tcg tta cct tct ggc gac aat gga	1162
Asp Thr Val Pro Thr Asn Thr Val Ser Leu Pro Ser Gly Asp Asn Gly	

71/88

360	365	370	
aaa tta ggt gga ttt aca cat gaa aat aac acc ata gat tcc gga gaa Lys Leu Gly Gly Phe Thr His Glu Asn Asn Thr Ile Asp Ser Gly Glu 375 380 385			1210
ctt gat att ggc cgg aga gca att caa gag gtt ccc ccc ggg atc ttc Leu Asp Ile Gly Arg Arg Ala Ile Gln Glu Val Pro Pro Gly Ile Phe 390 395 400			1258
tgg aga tcg cag ctc ttt att gat cag cca cag ttt ctt aag ttc aac Trp Arg Ser Gln Leu Phe Ile Asp Gln Pro Gln Phe Leu Lys Phe Asn 405 410 415			1306
atc tct ctt cag aag gat gca ttg atc gga gtg tac ggc cgg aag ggc Ile Ser Leu Gln Lys Asp Ala Leu Ile Gly Val Tyr Gly Arg Lys Gly 420 425 430 435			1354
tta ccg cct tcc cat act cag tac gac ttt gtg gaa cta ctg gat ggt Leu Pro Pro Ser His Thr Gln Tyr Asp Phe Val Glu Leu Leu Asp Gly 440 445 450			1402
agc agg tta att gcg aga gag cag cgg aac ctg gtg gag tcc gaa aga Ser Arg Leu Ile Ala Arg Glu Gln Arg Asn Leu Val Glu Ser Glu Arg 455 460 465			1450
gcc ggg cgg cag gcg aga tct gtc agc ctg cac gaa gct ggc ttc atc Ala Gly Arg Gln Ala Arg Ser Val Ser Leu His Glu Ala Gly Phe Ile 470 475 480			1498
cag tac ttg gat tct gga atc tgg cat ctg gct ttt tat aac gac ggg Gln Tyr Leu Asp Ser Gly Ile Trp His Leu Ala Phe Tyr Asn Asp Gly 485 490 495			1546
aaa aac cca gag cag gtc tcc ttt aac acg atc gtt ata gag tct gtg Lys Asn Pro Glu Gln Val Ser Phe Asn Thr Ile Val Ile Glu Ser Val 500 505 510 515			1594
gtg gaa tgc ccc cga aat tgc cat gga aat gga gag tgt gtt tct gga Val Glu Cys Pro Arg Asn Cys His Gly Asn Gly Glu Cys Val Ser Gly 520 525 530			1642
act tgc cat tgt ttc ccc ggg ttt cta ggt ccg gat tgt tca aga gca Thr Cys His Cys Phe Pro Gly Phe Leu Gly Pro Asp Cys Ser Arg Ala 535 540 545			1690
gcc tgt ccg gtg ctc tgt agt ggc aac ggg caa tac tcc aag ggc cgc Ala Cys Pro Val Leu Cys Ser Gly Asn Gly Gln Tyr Ser Lys Gly Arg 550 555 560			1738
tgc ctg tgc ttc agt ggc tgg aag ggc acc gag tgt gac gtg ccg acg Cys Leu Cys Phe Ser Gly Trp Lys Gly Thr Glu Cys Asp Val Pro Thr 565 570 575			1786
acc cag tgc att gac ccg cag tgc ggg ggt cgt ggg att tgc atc atg Thr Gln Cys Ile Asp Pro Gln Cys Gly Gly Arg Gly Ile Cys Ile Met 580 585 590 595			1834
ggc tct tgc gct tgt aac tcg gga tac aaa gga gaa aac tgt gag gaa			1882

72/88

Gly Ser Cys Ala Cys Asn Ser Gly Tyr Lys Gly Glu Asn Cys Glu Glu	
600 605 610	
gcg gac tgt cta gac cct gga tgt tct aat cac ggg gtg tgt atc cat	1930
Ala Asp Cys Leu Asp Pro Gly Cys Ser Asn His Gly Val Cys Ile His	
615 620 625	
ggg gaa tgt cac tgc aat cca ggc tgg ggt ggc agc aac tgt gaa ata	1978
Gly Glu Cys His Cys Asn Pro Gly Trp Gly Gly Ser Asn Cys Glu Ile	
630 635 640	
ctg aag act atg tgt gca gac cag tgc tca ggc cac ggg act tac ctt	2026
Leu Lys Thr Met Cys Ala Asp Gln Cys Ser Gly His Gly Thr Tyr Leu	
645 650 655	
caa gaa agc ggc tcc tgc act tgc gac cca aat tgg act ggc ccc gac	2074
Gln Glu Ser Gly Ser Cys Thr Cys Asp Pro Asn Trp Thr Gly Pro Asp	
660 665 670 675	
tgc tca aat gaa ata tgt tca gtg gac tgc ggc tca cac ggc gtc tgc	2122
Cys Ser Asn Glu Ile Cys Ser Val Asp Cys Gly Ser His Gly Val Cys	
680 685 690	
atg ggg ggc tcc tgt cgc tgt gaa gaa ggc tgg acc ggc ccg gcg tgt	2170
Met Gly Gly Ser Cys Arg Cys Glu Glu Gly Trp Thr Gly Pro Ala Cys	
695 700 705	
aat cag aga gct tgc cac cct cgc tgt gct gag cac ggg acg tgc aag	2218
Asn Gln Arg Ala Cys His Pro Arg Cys Ala Glu His Gly Thr Cys Lys	
710 715 720	
gac ggc aag tgc gag tgc agc caa gga tgg aac gga gag cac tgc aca	2266
Asp Gly Lys Cys Glu Cys Ser Gln Gly Trp Asn Gly Glu His Cys Thr	
725 730 735	
att gct cac tat ttg gat aag ata gtt aaa gag ggt tgc ccc ggc ttg	2314
Ile Ala His Tyr Leu Asp Lys Ile Val Lys Glu Gly Cys Pro Gly Leu	
740 745 750 755	
tgc aac agc aat ggg aga tgc aca ctg gac caa aac ggc tgg cac tgc	2362
Cys Asn Ser Asn Gly Arg Cys Thr Leu Asp Gln Asn Gly Trp His Cys	
760 765 770	
gtt tgc cag cca ggg tgg aga gga gca ggc tgt gac gta gcc atg gag	2410
Val Cys Gln Pro Gly Trp Arg Gly Ala Gly Cys Asp Val Ala Met Glu	
775 780 785	
acc ctc tgt aca gac agc aaa gac aac gaa gga gac gga ctc att gac	2458
Thr Leu Cys Thr Asp Ser Lys Asp Asn Glu Gly Asp Gly Leu Ile Asp	
790 795 800	
tgc atg gat cct gat tgc tgc ctc cag agc tcc tgc caa aac cag ccc	2506
Cys Met Asp Pro Asp Cys Cys Leu Gln Ser Ser Cys Gln Asn Gln Pro	
805 810 815	
tac tgt cgt ggc ttg cct gat cct cag gat atc att agc caa agc ctt	2554
Tyr Cys Arg Gly Leu Pro Asp Pro Gln Asp Ile Ile Ser Gln Ser Leu	
820 825 830 835	



73/88

cag aca cca tct cag caa gct gcc aag tcc ttc tat gac cga atc agt Gln Thr Pro Ser Gln Gln Ala Ala Lys Ser Phe Tyr Asp Arg Ile Ser 840 845 850	2602
ttc ctg att gga tcg gat agc acc cac gtg ctc cct gga gaa agt ccg Phe Leu Ile Gly Ser Asp Ser Thr His Val Leu Pro Gly Glu Ser Pro 855 860 865	2650
ttc aat aag agt ctt gcg tcc gtc atc aga ggc caa gta cta aca gct Phe Asn Lys Ser Leu Ala Ser Val Ile Arg Gly Gln Val Leu Thr Ala 870 875 880	2698
gat gga acc cca ctt att ggc gtc aac gtg tcg ttt tta cac tac tcg Asp Gly Thr Pro Leu Ile Gly Val Asn Val Ser Phe Leu His Tyr Ser 885 890 895	2746
gaa tat gga tat acc att acc cgc cag gat gga atg ttt gac ttg gtg Glu Tyr Gly Tyr Thr Ile Thr Arg Gln Asp Gly Met Phe Asp Leu Val 900 905 910 915	2794
gca aat ggt ggc gct tct ctg act ttg gta ttt gag cgt tcc cca ttc Ala Asn Gly Gly Ala Ser Leu Thr Leu Val Phe Glu Arg Ser Pro Phe 920 925 930	2842
ctc act cag tac cac act gtg tgg att ccc tgg aat gtc ttt tat gtg Leu Thr Gln Tyr His Thr Val Trp Ile Pro Trp Asn Val Phe Tyr Val 935 940 945	2890
atg gat acc ctt gtc atg aag aaa gag gag aac gac att ccc agc tgt Met Asp Thr Leu Val Met Lys Lys Glu Glu Asn Asp Ile Pro Ser Cys 950 955 960	2938
gac ctc agt ggc ttt gtg agg cca agt ccc atc att gtg tct tca ccg Asp Leu Ser Gly Phe Val Arg Pro Ser Pro Ile Ile Val Ser Ser Pro 965 970 975	2986
tta tcc acc ttc ttc agg tct tcc cct gag gac agc ccc atc atc ccc Leu Ser Thr Phe Phe Arg Ser Ser Pro Glu Asp Ser Pro Ile Ile Pro 980 985 990 995	3034
gag aca cag gtc ctg cat gaa gaa acc aca att cca gga aca gat Glu Thr Gln Val Leu His Glu Glu Thr Thr Ile Pro Gly Thr Asp 1000 1005 1010	3079
ttg aaa ctt tcc tac ctg agt tcc aga gcg gca ggg tac aag tca Leu Lys Leu Ser Tyr Leu Ser Ser Arg Ala Ala Gly Tyr Lys Ser 1015 1020 1025	3124
gtt ctt aag att acc atg acc cag gcc gtc ata ccg ttt aac ctc Val Leu Lys Ile Thr Met Thr Gln Ala Val Ile Pro Phe Asn Leu 1030 1035 1040	3169
atg aag gtc cat ctg atg gtg gcc gtg gtt ggg aga ctc ttc cag Met Lys Val His Leu Met Val Ala Val Val Gly Arg Leu Phe Gln 1045 1050 1055	3214
aag tgg ttt cct gcc tcg cca aac ttg gcc tac acg ttc atc tgg Lys Trp Phe Pro Ala Ser Pro Asn Leu Ala Tyr Thr Phe Ile Trp 1060 1065 1070	3259

74/88

gat aag acg gac gca	tat aat cag aaa gtc	tac ggc ttg tca gag	3304
Asp Lys Thr Asp Ala	Tyr Asn Gln Lys Val	Tyr Gly Leu Ser Glu	
1075	1080	1085	
gca gtt gtg tcc gtc	gga tac gag tac gag	tcg tgc ttg gac ctg	3349
Ala Val Val Ser Val	Gly Tyr Glu Tyr Glu	Ser Cys Leu Asp Leu	
1090	1095	1100	
act ctc tgg gaa aag	agg act gcc gtt ttg	caa ggc tat gag ttg	3394
Thr Leu Trp Glu Lys	Arg Thr Ala Val Leu	Gln Gly Tyr Glu Leu	
1105	1110	1115	
gat gct tcg aac atg	ggc ggc tgg acg ttg	gac aag cac cat gta	3439
Asp Ala Ser Asn Met	Gly Gly Trp Thr Leu	Asp Lys His His Val	
1120	1125	1130	
ctg gac gtt cag aac	ggg ata cta tac aaa	gga aat gga gaa aat	3484
Leu Asp Val Gln Asn	Gly Ile Leu Tyr Lys	Gly Asn Gly Glu Asn	
1135	1140	1145	
cag ttc atc tct cag	cag cct ccg gtg gtc	agc agc atc atg ggt	3529
Gln Phe Ile Ser Gln	Gln Pro Pro Val Val	Ser Ser Ile Met Gly	
1150	1155	1160	
aat ggt cgg agg cgt	agc atc tca tgc cca	agt tgc aat ggt caa	3574
Asn Gly Arg Arg Arg	Ser Ile Ser Cys Pro	Ser Cys Asn Gly Gln	
1165	1170	1175	
gct gac ggg aac aaa	ctc ctg gca ccc gtg	gcg ctt gcc tgt ggg	3619
Ala Asp Gly Asn Lys	Leu Leu Ala Pro Val	Ala Leu Ala Cys Gly	
1180	1185	1190	
atc gac ggc agt cta	tac gta ggg gat ttc	aat tac gtc cgg cgg	3664
Ile Asp Gly Ser Leu	Tyr Val Gly Asp Phe	Asn Tyr Val Arg Arg	
1195	1200	1205	
ata ttc ccg tct ggg	aat gtg aca agt gtt	tta gaa cta aga aat	3709
Ile Phe Pro Ser Gly	Asn Val Thr Ser Val	Leu Glu Leu Arg Asn	
1210	1215	1220	
aaa gat ttt aga cat	agt agc aac cca gct	cac aga tac tac ctg	3754
Lys Asp Phe Arg His	Ser Ser Asn Pro Ala	His Arg Tyr Tyr Leu	
1225	1230	1235	
gct acg gac cca gtc	acc gga gat ttg tac	gtc tct gat act aac	3799
Ala Thr Asp Pro Val	Thr Gly Asp Leu Tyr	Val Ser Asp Thr Asn	
1240	1245	1250	
acc cgc aga atc tat	cgg ccg aaa tca ctc	acg gga gcc aaa gac	3844
Thr Arg Arg Ile Tyr	Arg Pro Lys Ser Leu	Thr Gly Ala Lys Asp	
1255	1260	1265	
ctg act aaa aac gct	gaa gtg gtg gca ggg	acc ggg gaa cag tgc	3889
Leu Thr Lys Asn Ala	Glu Val Val Ala Gly	Thr Gly Glu Gln Cys	
1270	1275	1280	
ctt ccc ttt gac gag	gcc agg tgt ggg gat	gga ggc aag gct gtg	3934
Leu Pro Phe Asp Glu	Ala Arg Cys Gly Asp	Gly Gly Lys Ala Val	

75/88

1285	1290	1295	
gaa gca acg ctc atg Glu Ala Thr Leu Met 1300	agt ccc aaa gga atg Ser Pro Lys Gly Met 1305	gca atc gat aag aac Ala Ile Asp Lys Asn 1310	3979
gga ctg atc tac ttt Gly Leu Ile Tyr Phe 1315	gtt gat gga acc atg Val Asp Gly Thr Met 1320	atc aga aag gtt gat Ile Arg Lys Val Asp 1325	4024
caa aat gga atc ata Gln Asn Gly Ile Ile 1330	tca act ctc ctg ggc Ser Thr Leu Leu Gly 1335	tcc aac gac ctc acg Ser Asn Asp Leu Thr 1340	4069
tca gct cga cct tta Ser Ala Arg Pro Leu 1345	acc tgt gat act agc Thr Cys Asp Thr Ser 1350	atg cat atc agc cag Met His Ile Ser Gln 1355	4114
gtg cgt ctg gaa tgg Val Arg Leu Glu Trp 1360	ccc act gac ctc gcg Pro Thr Asp Leu Ala 1365	atc aac ccc atg gat Ile Asn Pro Met Asp 1370	4159
aac tcc atc tac gtc Asn Ser Ile Tyr Val 1375	ctg gat aat aac gta Leu Asp Asn Asn Val 1380	gtt tta cag atc act Val Leu Gln Ile Thr 1385	4204
gaa aac cgt cag gtc Glu Asn Arg Gln Val 1390	cgc atc gct gcc ggg Arg Ile Ala Ala Gly 1395	cgg ccc atg cac tgt Arg Pro Met His Cys 1400	4249
cag gtc cct gga gtg Gln Val Pro Gly Val 1405	gaa tac ccg gtg ggg Glu Tyr Pro Val Gly 1410	aag cac gcg gtt cag Lys His Ala Val Gln 1415	4294
acc acc ctg gag tca Thr Thr Leu Glu Ser 1420	gcc acg gcc att gct Ala Thr Ala Ile Ala 1425	gtg tcc tac agc ggg Val Ser Tyr Ser Gly 1430	4339
gtc ctt tac atc acg Val Leu Tyr Ile Thr 1435	gaa act gat gag aag Glu Thr Asp Glu Lys 1440	aag atc aac cga ata Lys Ile Asn Arg Ile 1445	4384
agg cag gtc acg aca Arg Gln Val Thr Thr 1450	gac ggg gag atc tcc Asp Gly Glu Ile Ser 1455	tta gtg gct ggg ata Leu Val Ala Gly Ile 1460	4429
cct tcg gaa tgt gac Pro Ser Glu Cys Asp 1465	tgc aag aac gac gcc Cys Lys Asn Asp Ala 1470	aac tgt gac tgc tac Asn Cys Asp Cys Tyr 1475	4474
caa agc gga gac ggc Gln Ser Gly Asp Gly 1480	tac gcc aaa gat gcc Tyr Ala Lys Asp Ala 1485	aaa ctc aat gcg ccg Lys Leu Asn Ala Pro 1490	4519
tcc tcc ctg gcc gcc Ser Ser Leu Ala Ala 1495	tcg cca gat ggc act Ser Pro Asp Gly Thr 1500	ctg tac att gca gat Leu Tyr Ile Ala Asp 1505	4564
ctg gga aat atc agg	atc cgg gcc gtt tcg	aag aat aaa cct tta	4609

76/88

Leu Gly Asn Ile Arg	Ile Arg Ala Val Ser	Lys Asn Lys Pro Leu	
1510	1515	1520	
ctg aac tca atg aac	ttt tac gaa gtt gcc	tct cca act gat caa	4654
Leu Asn Ser Met Asn	Phe Tyr Glu Val Ala	Ser Pro Thr Asp Gln	
1525	1530	1535	
gag ctc tac atc ttt	gac atc aac ggt act	cac cag tac acc gtg	4699
Glu Leu Tyr Ile Phe	Asp Ile Asn Gly Thr	His Gln Tyr Thr Val	
1540	1545	1550	
agc ctg gtc acg ggt	gac tac cta tat aat	ttt agt tac agc aat	4744
Ser Leu Val Thr Gly	Asp Tyr Leu Tyr Asn	Phe Ser Tyr Ser Asn	
1555	1560	1565	
gac aat gac gtc acc	gct gta act gac agc	aat ggc aac acc ctc	4789
Asp Asn Asp Val Thr	Ala Val Thr Asp Ser	Asn Gly Asn Thr Leu	
1570	1575	1580	
cga atc cga agg gat	ccg aat cgg atg ccg	gtg cgg gtg gtg tct	4834
Arg Ile Arg Arg Asp	Pro Asn Arg Met Pro	Val Arg Val Val Ser	
1585	1590	1595	
cct gat aac cag gtg	ata tgg ttg acc ata	ggc acc aac ggg tgt	4879
Pro Asp Asn Gln Val	Ile Trp Leu Thr Ile	Gly Thr Asn Gly Cys	
1600	1605	1610	
ctg aaa agc atg acc	gct cag ggc ctg gaa	ctg gtt ttg ttt act	4924
Leu Lys Ser Met Thr	Ala Gln Gly Leu Glu	Leu Val Leu Phe Thr	
1615	1620	1625	
tac cat ggc aac agt	ggg ctt tta gcc acc	aaa agt gac gaa act	4969
Tyr His Gly Asn Ser	Gly Leu Leu Ala Thr	Lys Ser Asp Glu Thr	
1630	1635	1640	
gga tgg aca aca ttt	ttt gac tat gac agt	gaa ggt cgc ctg acg	5014
Gly Trp Thr Thr Phe	Phe Asp Tyr Asp Ser	Glu Gly Arg Leu Thr	
1645	1650	1655	
aat gtt acc ttc ccc	act ggg gtg gtt aca	aac ctg cac ggg gac	5059
Asn Val Thr Phe Pro	Thr Gly Val Val Thr	Asn Leu His Gly Asp	
1660	1665	1670	
atg gac aag gct atc	acg gtg gac atc gag	tca tcc agc aga gag	5104
Met Asp Lys Ala Ile	Thr Val Asp Ile Glu	Ser Ser Ser Arg Glu	
1675	1680	1685	
gaa gat gtc agc atc	act tcg aac ttg tcc	tcc atc gat tcc ttc	5149
Glu Asp Val Ser Ile	Thr Ser Asn Leu Ser	Ser Ile Asp Ser Phe	
1690	1695	1700	
tac acc atg gtc caa	gac cag tta aga aac	agt tac cag att ggg	5194
Tyr Thr Met Val Gln	Asp Gln Leu Arg Asn	Ser Tyr Gln Ile Gly	
1705	1710	1715	
tat gat ggc tcc ctt	aga atc ttc tat gcc	agt ggt ctg gac tct	5239
Tyr Asp Gly Ser Leu	Arg Ile Phe Tyr Ala	Ser Gly Leu Asp Ser	
1720	1725	1730	

77/88

cac tac cag aca gag	ccc cac gtt ctg gct	ggc acg gcg aat ccc	5284
His Tyr Gln Thr Glu	Pro His Val Leu Ala	Gly Thr Ala Asn Pro	
1735	1740	1745	
aca gta gcc aaa aga	aac atg act ctt ccc	ggt gag aac ggg cag	5329
Thr Val Ala Lys Arg	Asn Met Thr Leu Pro	Gly Glu Asn Gly Gln	
1750	1755	1760	
aat ctg gtg gag tgg	aga ttc cga aaa gaa	caa gcc cag ggc aaa	5374
Asn Leu Val Glu Trp	Arg Phe Arg Lys Glu	Gln Ala Gln Gly Lys	
1765	1770	1775	
gtc aac gta ttc ggc	cgg aag ctc agg gtc	aat ggg cgc aac cta	5419
Val Asn Val Phe Gly	Arg Lys Leu Arg Val	Asn Gly Arg Asn Leu	
1780	1785	1790	
ctc tca gtg gac ttt	gat cgg acc acc aag	acg gaa aag atc tat	5464
Leu Ser Val Asp Phe	Asp Arg Thr Thr Lys	Thr Glu Lys Ile Tyr	
1795	1800	1805	
gat gac cac cgg aaa	ttt ctc ctg agg atc	gct tac gac acg tcg	5509
Asp Asp His Arg Lys	Phe Leu Leu Arg Ile	Ala Tyr Asp Thr Ser	
1810	1815	1820	
ggg cac ccg act ctc	tgg ctg ccg agt agc	aag cta atg gca gtg	5554
Gly His Pro Thr Leu	Trp Leu Pro Ser Ser	Lys Leu Met Ala Val	
1825	1830	1835	
aac gtc acc tac tca	tcc acc ggt caa att	gcc agc atc cag aga	5599
Asn Val Thr Tyr Ser	Ser Thr Gly Gln Ile	Ala Ser Ile Gln Arg	
1840	1845	1850	
ggg acc acg agc gaa	aag gtg gac tat gac	agc cag ggg agg atc	5644
Gly Thr Thr Ser Glu	Lys Val Asp Tyr Asp	Ser Gln Gly Arg Ile	
1855	1860	1865	
gta tct cgg gtc ttt	gcc gat ggg aaa aca	tgg agt tac acg tac	5689
Val Ser Arg Val Phe	Ala Asp Gly Lys Thr	Trp Ser Tyr Thr Tyr	
1870	1875	1880	
ttg gaa aag tcc atg	gtt ctt ctg ctc cat	agc cag cgg cag tac	5734
Leu Glu Lys Ser Met	Val Leu Leu Leu His	Ser Gln Arg Gln Tyr	
1885	1890	1895	
atc ttc gaa tac gac	atg tgg gac cgc ctg	tcc gcc atc acc atg	5779
Ile Phe Glu Tyr Asp	Met Trp Asp Arg Leu	Ser Ala Ile Thr Met	
1900	1905	1910	
ccc agt gtg gct cgc	cac acc atg cag acc	atc cgg tcc att ggc	5824
Pro Ser Val Ala Arg	His Thr Met Gln Thr	Ile Arg Ser Ile Gly	
1915	1920	1925	
tac tac cgc aac atc	tac aat ccc cca gaa	agc aat gcc tct atc	5869
Tyr Tyr Arg Asn Ile	Tyr Asn Pro Pro Glu	Ser Asn Ala Ser Ile	
1930	1935	1940	
atc acc gac tac aac	gag gaa ggg ctg ctt	ctg caa aca gct ttc	5914
Ile Thr Asp Tyr Asn	Glu Glu Gly Leu Leu	Leu Gln Thr Ala Phe	
1945	1950	1955	

78/88

ctg gga acg agt cgg	agg gtc tta ttc aag	tat aga agg cag acc	5959
Leu Gly Thr Ser Arg	Arg Val Leu Phe Lys	Tyr Arg Arg Gln Thr	
1960	1965	1970	
agg cta tca gaa att	tta tac gac agc aca	aga gtc agt ttt acc	6004
Arg Leu Ser Glu Ile	Leu Tyr Asp Ser Thr	Arg Val Ser Phe Thr	
1975	1980	1985	
tac gac gaa aca gcg	gga gtc ctg aaa aca	gta aac ctt cag agt	6049
Tyr Asp Glu Thr Ala	Gly Val Leu Lys Thr	Val Asn Leu Gln Ser	
1990	1995	2000	
gat ggt ttt att tgc	acc att aga tac agg	caa att ggt ccc ctg	6094
Asp Gly Phe Ile Cys	Thr Ile Arg Tyr Arg	Gln Ile Gly Pro Leu	
2005	2010	2015	
att gac aga cag att	ttc cgc ttc agc gag	gat gga atg gta aat	6139
Ile Asp Arg Gln Ile	Phe Arg Phe Ser Glu	Asp Gly Met Val Asn	
2020	2025	2030	
gcg aga ttt gac tat	agc tac gac aac agc	ttt cga gtg acc agc	6184
Ala Arg Phe Asp Tyr	Ser Tyr Asp Asn Ser	Phe Arg Val Thr Ser	
2035	2040	2045	
atg cag ggt gtc atc	aat gaa aca cca ctg	ccc att gat cta tac	6229
Met Gln Gly Val Ile	Asn Glu Thr Pro Leu	Pro Ile Asp Leu Tyr	
2050	2055	2060	
cag ttt gat gac atc	tct ggc aaa gtc gag	cag ttt gga aaa ttc	6274
Gln Phe Asp Asp Ile	Ser Gly Lys Val Glu	Gln Phe Gly Lys Phe	
2065	2070	2075	
gga gtg ata tac tac	gac atc aac caa atc	att tcc acg gcc gtg	6319
Gly Val Ile Tyr Tyr	Asp Ile Asn Gln Ile	Ile Ser Thr Ala Val	
2080	2085	2090	
atg act tat aca aag	cac ttt gat gct cat	ggg cgc atc aag gag	6364
Met Thr Tyr Thr Lys	His Phe Asp Ala His	Gly Arg Ile Lys Glu	
2095	2100	2105	
atc caa tat gag ata	ttt agg tca ctc atg	tac tgg att aca att	6409
Ile Gln Tyr Glu Ile	Phe Arg Ser Leu Met	Tyr Trp Ile Thr Ile	
2110	2115	2120	
caa tat gat aat atg	ggc cgg gta acc aag	aga gag att aaa att	6454
Gln Tyr Asp Asn Met	Gly Arg Val Thr Lys	Arg Glu Ile Lys Ile	
2125	2130	2135	
ggg cct ttt gcc aac	act acc aaa tac gcg	tac gag tac gac gtc	6499
Gly Pro Phe Ala Asn	Thr Thr Lys Tyr Ala	Tyr Glu Tyr Asp Val	
2140	2145	2150	
gat gga cag ctc caa	aca gtt tac cta aac	gaa aag atc atg tgg	6544
Asp Gly Gln Leu Gln	Thr Val Tyr Leu Asn	Glu Lys Ile Met Trp	
2155	2160	2165	
cgg tac aac tac gac	cta aat gga aac ctc	cac ttg ctc aac ccc	6589
Arg Tyr Asn Tyr Asp	Leu Asn Gly Asn Leu	His Leu Leu Asn Pro	

79/88

2170	2175	2180	
agc agc agc gcc cgc	ctg acc cct ctg cgc	tat gac ctg cgc gac	6634
Ser Ser Ser Ala Arg	Leu Thr Pro Leu Arg	Tyr Asp Leu Arg Asp	
2185	2190	2195	
aga atc acc cgc ctg	ggc gat gtt cag tac	cgg ctg gat gaa gat	6679
Arg Ile Thr Arg Leu	Gly Asp Val Gln Tyr	Arg Leu Asp Glu Asp	
2200	2205	2210	
ggt ttc ctg cgt cag	agg ggc act gaa att	ttt gaa tac agc tcc	6724
Gly Phe Leu Arg Gln	Arg Gly Thr Glu Ile	Phe Glu Tyr Ser Ser	
2215	2220	2225	
aaa ggg ctt ctg act	cga gtc tac agt aaa	ggc agt ggc tgg aca	6769
Lys Gly Leu Leu Thr	Arg Val Tyr Ser Lys	Gly Ser Gly Trp Thr	
2230	2235	2240	
gtg atc tat cgg tac	gac ggc ctg gga aga	cgt gtt tct agc aaa	6814
Val Ile Tyr Arg Tyr	Asp Gly Leu Gly Arg	Arg Val Ser Ser Lys	
2245	2250	2255	
acc agc ctg gga cag	cac ctt cag ttt ttc	tac gcc gac ctg aca	6859
Thr Ser Leu Gly Gln	His Leu Gln Phe Phe	Tyr Ala Asp Leu Thr	
2260	2265	2270	
tac ccc acg aga att	act cac gtc tac aac	cat tcc agt tca gaa	6904
Tyr Pro Thr Arg Ile	Thr His Val Tyr Asn	His Ser Ser Ser Glu	
2275	2280	2285	
atc acc tcc ctg tac	tat gac ctc caa gga	cat ctc ttc gcc atg	6949
Ile Thr Ser Leu Tyr	Tyr Asp Leu Gln Gly	His Leu Phe Ala Met	
2290	2295	2300	
gag atc agc agt ggg	gat gag ttc tac atc	gcc tcg gac aac acg	6994
Glu Ile Ser Ser Gly	Asp Glu Phe Tyr Ile	Ala Ser Asp Asn Thr	
2305	2310	2315	
ggg aca ccg ctg gct	gtt ttc agc agc aac	ggg ctc atg ctg aaa	7039
Gly Thr Pro Leu Ala	Val Phe Ser Ser Asn	Gly Leu Met Leu Lys	
2320	2325	2330	
cag acc cag tac act	gcc tat ggt gag atc	tac ttt gac tcc aac	7084
Gln Thr Gln Tyr Thr	Ala Tyr Gly Glu Ile	Tyr Phe Asp Ser Asn	
2335	2340	2345	
gtc gac ttt cag ctg	gta att gga ttc cac	ggg ggc ttg tat gac	7129
Val Asp Phe Gln Leu	Val Ile Gly Phe His	Gly Gly Leu Tyr Asp	
2350	2355	2360	
ccg ctc acc aaa cta	atc cac ttt gga gaa	aga gat tat gac att	7174
Pro Leu Thr Lys Leu	Ile His Phe Gly Glu	Arg Asp Tyr Asp Ile	
2365	2370	2375	
ttg gcg gga aga tgg	acc aca ccg gac att	gaa atc tgg aaa agg	7219
Leu Ala Gly Arg Trp	Thr Thr Pro Asp Ile	Glu Ile Trp Lys Arg	
2380	2385	2390	
atc gga aag gac cct	gct cct ttt aac ctg	tat atg ttt cgg aat	7264

80/88

Ile Gly Lys Asp Pro	Ala Pro Phe Asn Leu	Tyr Met Phe Arg Asn	
2395	2400	2405	
aac aac ccc gcg agc	aaa atc cat gat gtg	aaa gat tac atc acg	7309
Asn Asn Pro Ala Ser	Lys Ile His Asp Val	Lys Asp Tyr Ile Thr	
2410	2415	2420	
gat gtt aac agc tgg	ctg gtg acg ttt ggc	ttc cat ctg cac aat	7354
Asp Val Asn Ser Trp	Leu Val Thr Phe Gly	Phe His Leu His Asn	
2425	2430	2435	
gct att cct gga ttc	cct gtt ccc aaa ttt	gat tta act gag cct	7399
Ala Ile Pro Gly Phe	Pro Val Pro Lys Phe	Asp Leu Thr Glu Pro	
2440	2445	2450	
tcc tat gag ctt gtg	aag agt caa cag tgg	gaa gat gtg ccg ccc	7444
Ser Tyr Glu Leu Val	Lys Ser Gln Gln Trp	Glu Asp Val Pro Pro	
2455	2460	2465	
atc ttt gga gtt cag	cag caa gtg gca agg	caa gcc aag gcc ttc	7489
Ile Phe Gly Val Gln	Gln Gln Val Ala Arg	Gln Ala Lys Ala Phe	
2470	2475	2480	
ttg tcc ctg ggg aag	atg gcc gag gtg cag	gtg agc cga cgc aaa	7534
Leu Ser Leu Gly Lys	Met Ala Glu Val Gln	Val Ser Arg Arg Lys	
2485	2490	2495	
gct ggc gcc gag cag	tcg tgg ctg tgg ttc	gcc acg gtc aag tcg	7579
Ala Gly Ala Glu Gln	Ser Trp Leu Trp Phe	Ala Thr Val Lys Ser	
2500	2505	2510	
ctc atc ggc aag ggc	gtc atg ctg gcc gtg	agc caa ggc cgc gtg	7624
Leu Ile Gly Lys Gly	Val Met Leu Ala Val	Ser Gln Gly Arg Val	
2515	2520	2525	
cag acc aac gtg ctc	aac atc gcc aac gag	gac tgc atc aag gtg	7669
Gln Thr Asn Val Leu	Asn Ile Ala Asn Glu	Asp Cys Ile Lys Val	
2530	2535	2540	
gcg gcg gtg ctc aac	aac gcc ttc tac ctg	gag aac ctg cac ttc	7714
Ala Ala Val Leu Asn	Asn Ala Phe Tyr Leu	Glu Asn Leu His Phe	
2545	2550	2555	
acc atc gag ggc aag	gac aca cac tac ttc	atc aag acc acc aca	7759
Thr Ile Glu Gly Lys	Asp Thr His Tyr Phe	Ile Lys Thr Thr Thr	
2560	2565	2570	
ccc gag agc gac ctg	ggc aca ctg cgg ctg	acg agc ggt cgc aag	7804
Pro Glu Ser Asp Leu	Gly Thr Leu Arg Leu	Thr Ser Gly Arg Lys	
2575	2580	2585	
gcc ctg gag aac ggg	atc aac gtg acc gtg	tct cag tcc acc acg	7849
Ala Leu Glu Asn Gly	Ile Asn Val Thr Val	Ser Gln Ser Thr Thr	
2590	2595	2600	
gtg gtg aac ggc agg	act cgc agg ttc gcc	gac gtg gag atg cag	7894
Val Val Asn Gly Arg	Thr Arg Arg Phe Ala	Asp Val Glu Met Gln	
2605	2610	2615	



81/88

ttc ggt gcc ctg gca	ctg cat gtg cgc tat	ggc atg acg ctg gac	7939
Phe Gly Ala Leu Ala	Leu His Val Arg Tyr	Gly Met Thr Leu Asp	
2620	2625	2630	
gag gag aag gcg cgc	att ctg gag cag gcg	cgc cag cgc gcg ctc	7984
Glu Glu Lys Ala Arg	Ile Leu Glu Gln Ala	Arg Gln Arg Ala Leu	
2635	2640	2645	
gcc cgg gcg tgg gca	cgg gag cag cag cgc	gtg cgc gac ggc gag	8029
Ala Arg Ala Trp Ala	Arg Glu Gln Gln Arg	Val Arg Asp Gly Glu	
2650	2655	2660	
gag ggt gcg cgc ctc	tgg acg gag ggt gag	aaa cgg cag ctg ctg	8074
Glu Gly Ala Arg Leu	Trp Thr Glu Gly Glu	Lys Arg Gln Leu Leu	
2665	2670	2675	
agc gct ggc aag gtg	cag ggc tac gat ggg	tac tac gta ctg tcg	8119
Ser Ala Gly Lys Val	Gln Gly Tyr Asp Gly	Tyr Tyr Val Leu Ser	
2680	2685	2690	
gtg gag cag tac ccc	gag ctg gct gac agt	gcc aac aac atc cag	8164
Val Glu Gln Tyr Pro	Glu Leu Ala Asp Ser	Ala Asn Asn Ile Gln	
2695	2700	2705	
ttc ttg cga caa agt	gag atc ggc aag agg	taa cccccgggcc	8207
Phe Leu Arg Gln Ser	Glu Ile Gly Lys Arg		
2710	2715		
acccctgtgc agattctcct	gtagcacaat ccaaaccgga	ctctccaaag agccttccaa	8267
aatgacactg ctctgcagac	agacacatcg cagatacaca	cgcaacacaa accagaaaca	8327
aagacaactt tttttttttt	ctgaatgacc ttaaagggtga	tcggcttttaa agaatatggt	8387
tacatacgca tatcgctgca	ctcaattgga ctggaagtat	gagaaaggaa aaaaaagcat	8447
taaaaaaggc aacgttttgc	catgaccctt ctgtaccttc	gaggcactgt atttaacaaa	8507
ggttttataaa aggaataaaa	aatgcgtaca atgtttccag	atattactga attgtcgacc	8567
tttgcttaca ggaagtaatc	tctacttagg atgtgatata	tatagatctg ttcatttttaa	8627
aatgtggggc aaagttactg	tttatagaac ccaactgctt	tcccgtgctg ctttgtaaaa	8687
ggacactggc acaagggacg	tctgcttcgg cggggattta	ataatggatt ttactaacat	8747
ggcttgccct gggagggaaa	aactgacgaa tagaatcctt	gtcactgata agcaaaggaa	8807
accctgattt ttttgtaaat	tatgtgagac aagttgttta	tggattttta tatgaattac	8867
aatttactgt acatcaaata	ttagtctcag aggagttaat	ttatgtaaag tgtttaaaaa	8927
gtttatactt aaaaataaaa	tgataaaaac aaaaaaa		8964

&lt;210&gt; 133

&lt;211&gt; 2253

82/88

<212> DNA

<213> Homo sapiens

**<220>**

<221> exon

<222> (107) . . (1090)

<223>

[illegible]

83/88

att tcc tcc aag gtg ccc aag gct gag tac atc ccc act atc atc cgc Ile Ser Ser Lys Val Pro Lys Ala Glu Tyr Ile Pro Thr Ile Ile Arg 150 155 160	595
cgg gat gac ccc tcc atc atc ccc atc ctc tac gac cat gag cac gca Arg Asp Asp Pro Ser Ile Ile Pro Ile Leu Tyr Asp His Glu His Ala 165 170 175	643
acc ttc gag gac atc ctt gag gag ata gag agg aag ctg aac gtc tac Thr Phe Glu Asp Ile Leu Glu Glu Ile Glu Arg Lys Leu Asn Val Tyr 180 185 190 195	691
cac aag gga gcc aag atc tgg aaa atg ctg att ttc tgc cag gga ggt His Lys Gly Ala Lys Ile Trp Lys Met Leu Ile Phe Cys Gln Gly Gly 200 205 210	739
cct gga cac ctc tat ctc ctc aag aac aag gtg gcc acc ttt gcc aaa Pro Gly His Leu Tyr Leu Leu Lys Asn Lys Val Ala Thr Phe Ala Lys 215 220 225	787
gtg gag aag gaa gag gac atg att cac ttc tgg aag cgg ctg agc cgc Val Glu Lys Glu Glu Asp Met Ile His Phe Trp Lys Arg Leu Ser Arg 230 235 240	835
ctg atg agc aaa gtg aac cca gag cgc aac gtc atc cac atc atg ggc Leu Met Ser Lys Val Asn Pro Glu Pro Asn Val Ile His Ile Met Gly 245 250 255	883
tgc tac att ctg ggg aac ccc aat gga gag aag ctg ttc cag aac ctc Cys Tyr Ile Leu Gly Asn Pro Asn Gly Glu Lys Leu Phe Gln Asn Leu 260 265 270 275	931
agg acc ctc atg act cct tat agg gtc acc ttc gag tca ccc ctg gag Arg Thr Leu Met Thr Pro Tyr Arg Val Thr Phe Glu Ser Pro Leu Glu 280 285 290	979
ctc tca gcc caa ggg aag cag atg atc gag acg tac ttt gac ttc cgg Leu Ser Ala Gln Gly Lys Gln Met Ile Glu Thr Tyr Phe Asp Phe Arg 295 300 305	1027
ttg tat cgc ctg tgg aag agc cgc cag cac tcg aag ctg ctg gac ttt Leu Tyr Arg Leu Trp Lys Ser Arg Gln His Ser Lys Leu Leu Asp Phe 310 315 320	1075
gac gac gtc ctg tga ggggcagagg cctccgccca gtcaccatca ggccactccc Asp Asp Val Leu 325	1130
tctgcaccgg gacctggggc tgggcccgcct cgtgctcccc gggactgtgt agctccggtc	1190
tcgcctggag ccacttcagg gcacctcaga cgttgctcag gttccccctg tgggttccgg	1250
tcctcgctgc acccgtggcc gcagaggctg cagtccctgg gggccgggag gatccccgcc	1310
tgtggcccggt ggatgctcag cggccaggca ctgacctgcc atgcctcgcc tggaggctca	1370
gctgtgggca tccctccatg gggttcatag aaataagtgc aatttctaca cccccgaaac	1430
aattcaaagg gaagcagcat ttcttggttaa ctagttaagc actatgctgc tagttacagt	1490

84/88

```

gtaggcaccc cggcccagca gccagcagc ccacatgtgt tcaggaccct ccctgcccac 1550
ccccccctg ccgtatcgat caccagcacc aggggtggccc gtgtgcgtgg ggccagcgtc 1610
gccgggctgc ccagcctggc tctgtctaca ctggccgagt ctctgggtct gtctacactg 1670
gccgagtctc cgactgtctg tgcttttact tacactcctc ttgccacccc ccatccctgc 1730
ttacttagac ctcagccggc gccggacccg gtaggggagc tctgggcagc aggaaggaag 1790
ggcgagcgt cccctccttc agaggaggct ctgggtgggg cctgctcctc atccccccaa 1850
gccaccccag cactctcatt gctgctgttg agttcagctt ttaccagcct cagtgtggag 1910
gctccatccc agcacacagg cctggggctt ggccaggggc cagctggggc tgggccctgg 1970
gttttgagaa actcgctggc accacagtgg gccctggac ccggccgcgc agctgggtgga 2030
ctgtaggggc tcctgactgg gcacaggagc tcccagcttt tgtccacggc cagcaggatg 2090
ggctgtcgtg tatatagctg gggcgagggg gcaggccccc cttgtgcaga gccaggggtc 2150
tgagggcacc tggctgtgtt cccagctgag ggagggtgg ggccgggggc gggcttgaa 2210
cgatgtacga taccctcata gtgaccatta aacctgatcc tcc 2253

```

&lt;210&gt; 134

&lt;211&gt; 2253

&lt;212&gt; DNA

&lt;213&gt; Danio rerio

&lt;220&gt;

&lt;221&gt; exon

&lt;222&gt; (1)..(298)

&lt;223&gt;

```

<400> 134
gtg ccc cgg atg tgc cca gct ggc tcc tgg ccc cac ccc tcg ggc ctt 48
Val Pro Arg Met Cys Pro Ala Gly Ser Trp Pro His Pro Ser Gly Leu
1 5 10 15

tgg gct gga cca gcc acc tct gcc tga gac ctc cgg tcg ccg caa gaa 96
Trp Ala Gly Pro Ala Thr Ser Ala Asp Leu Arg Ser Pro Gln Glu
20 25 30

gct gga gag gat gta cag cgt tga ccg tgt gtc tga cga cat ccc tat 144
Ala Gly Glu Asp Val Gln Arg Pro Cys Val Arg His Pro Tyr

```

85/88

35	40	45	
tcg tac ctg gtt ccc caa gga aaa tct ttt cag ctt cca gac agc aac			192
Ser Tyr Leu Val Pro Gln Gly Lys Ser Phe Gln Leu Pro Asp Ser Asn			
50	55	60	
cac aac tat gca agc ggt gtt cag ggg cta cgc gga gag gaa gcg ccg			240
His Asn Tyr Ala Ser Gly Val Gln Gly Leu Arg Gly Glu Glu Ala Pro			
65	70	75	
gaa acg gga gaa tga ttc cgc gtc tgt aat cca gag gaa ctt ccg caa			288
Glu Thr Gly Glu Phe Arg Val Cys Asn Pro Glu Glu Leu Pro Gln			
80	85	90	
aca cct gcg c atggtcggca gccggagggt gaaggcccag acgttcgctg			338
Thr Pro Ala			
95			
agcggcgcgca gcggagcttc agccgggtcct ggagcgaccc ccccccatg aaagccgaca			398
cttcccacga ctcccagac agcagtgacc tgcagagctc cactgcacg ctggacgagg			458
ccttcgagga cctggactgg gacactgaga agggcctgga ggctgtggcc tgcgacaccg			518
aaggcttcgt gccaccaaag gtcattgtca tttcctccaa ggtgcccag gctgagtaca			578
tccccactat catccgcgg gatgaccct ccatcatccc catcctctac gaccatgagc			638
acgcaacctt cgaggacatc cttgaggaga tagagaggaa gctgaacgtc taccacaagg			698
gagccaagat ctggaaaatg ctgattttct gccagggagg tcctggacac ctctatctcc			758
tcaagaacaa ggtggccacc tttgccaaag tggagaagga agaggacatg attcacttct			818
ggaagcggct gagccgcctg atgagcaaag tgaaccaga gccgaacgtc atccacatca			878
tgggctgcta cattctgggg aacccaatg gagagaagct gttccagaac ctgaggaccc			938
tcatgactcc ttatagggtc accttcgagt caccctgga gctctcagcc caagggaagc			998
agatgatcga gacgtacttt gacttccggt tgtatcgct gtggaagagc cgccagcact			1058
cgaagctgct ggactttgac gacgtcctgt gaggggcaga ggcctccgcc cagtcacat			1118
caggccactc cctctgcacc gggacctggg gctgggccc ctcgtgctcc ccgggactgt			1178
gtagctccgg tctcgccctg agccacttca gggcacctca gacgttgctc aggttcccc			1238
tgtgggttcc ggtcctcgct gcaccctgg cgcagaggc tgcagtcctt gggggccggg			1298
aggatccgc cctgtggccc gtggatgctc agcggccagg cactgacctg ccatgcctcg			1358
cctggaggct cagctgtggg catccctcca tggggttcat agaaataagt gcaatttcta			1418
cacccccgaa acaattcaaa gggaagcagc atttcttggt aactagttaa gcaactatgct			1478
gctagttaca gtgtaggcac cccggcccag cagcccagca gccacatgt gttcaggacc			1538
ctccctgccc acccctccc tgccgtatcg atcaccagca ccagggtggc ccgtgtgcgt			1598

86/88

ggggccagcg tcgccgggct gccagcctg gctctgtcta cactggccga gtctctgggt 1658  
ctgtctacac tggccgagtc tccgactgtc tgtgctttca cttacactcc tcttgccacc 1718  
ccccatccct gcttacttag acctcagccg gcgccggacc cggtaggggc agtctgggca 1778  
gcaggaagga agggcgagc gtccctcct tcagaggagg ctctgggtgg ggcctgctcc 1838  
tcatcccccc aagcccaccc agcactctca ttgctgctgt tgagttcagc ttttaccagc 1898  
ctcagtgtgg aggctccatc ccagcacaca ggcctggggc ttggcagggg cccagctggg 1958  
gctgggccct ggggttttgag aaactcgctg gcaccacagt gggcccctgg acccggcgc 2018  
gcagctggtg gactgtaggg gctcctgact gggcacagga gctcccagct tttgtccacg 2078  
gccagcagga tgggctgtcg tgtatatagc tggggcgagg gggcaggccc cccttgtgca 2138  
gagccagggg tctgaggga cctggctgtg ttcccagctg agggaggggt ggggcggggg 2198  
ccgggcttgg aacgatgtac gataccctca tagtgacat taaacctgat cctcc 2253

&lt;210&gt; 135

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; TCAP 3 General Motif

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (5)..(5)

&lt;223&gt; X=G, S or A

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (6)..(6)

&lt;223&gt; X=G or R

&lt;220&gt;

87/88

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (9) .. (9)

&lt;223&gt; X=L or Q

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (19) .. (19)

&lt;223&gt; X=V or I

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (32) .. (32)

&lt;223&gt; X=V or I

&lt;400&gt; 135

Gln	Leu	Leu	Ser	Xaa	Xaa	Lys	Val	Xaa	Gly	Tyr	Asp	Gly	Tyr	Tyr	Val
1				5					10					15	

Leu	Ser	Xaa	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn	Xaa
			20					25					30		

Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile
		35					40

&lt;210&gt; 136

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; G. gallus TCAP2

&lt;400&gt; 136

88/88

Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr	Val	Leu	Pro	Val	Glu
1				5					10					15	

Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn	Ile	Gln	Phe	Leu	Arg
			20					25					30		

Gln	Asn	Glu	Met
		35	